

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 02:31:42 : Search time 180.75 seconds
(without alignments)
2290.944 Million cell updates/sec

Title: us-09-525-998a-1_copy_121_603

Perfect score: 483

Sequence: 1 gatattgtgttcccaagg.....gctacccacgattggaat 483

Scoring table: IDENTITY_NUC

Gapop 10.0 : Gapext 1.0

Searched: 930621 seqs, 42962619 residues

Total number of hits satisfying chosen parameters: 1461347

Minimum DB seq length: 0

Maximum DB seq length: 2900000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_1101.*
1: /SID2/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SID2/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SID2/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SID2/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /SID2/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SID2/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /SID2/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /SID2/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /SID2/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /SID2/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SID2/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SID2/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SID2/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SID2/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /SID2/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /SID2/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SID2/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SID2/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SID2/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq/NA2001.DAT.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	483	100.0	483	19	Human soluble tumo
2	483	100.0	483	19	Soluble tumour nec
3	483	100.0	483	20	Tumour necrosis in
4	483	100.0	483	22	Human 30 kDa TNF
5	483	100.0	1301	18	cDNA for TNF(2019
6	483	100.0	1334	11	Plasmid tumour nec
7	483	100.0	1368	14	Lambda-derived TNF
8	483	100.0	1464	21	Human TNF1 coding
9	483	100.0	1478	20	CadC-tumour polyep
10	483	100.0	2062	13	TNF-alpha binding
11	483	100.0	2062	13	Encodes TNF-alpha

12	483	100.0	2088	12	AAQ19883	483: INF inhibitor
13	483	100.0	2088	22	AAQ83946	Human 30 kDa TNF
14	483	100.0	2111	12	AAQ23481	Human 30 kDa TNF
15	483	100.0	2111	20	AAQ99179	Human tumour necro
16	483	100.0	2161	21	AAZ48475	Human tumour necro
17	483	100.0	2175	16	AAQ90513	p55 TNF-R gene, H
18	483	100.0	6889	17	AAQ15931	Human TNF(2019
19	483	100.0	6926	18	AAQ03431	Vector pCDNA3-193
20	481.4	99.7	2141	11	AAQ06285	Human Tumour Necro
21	481.4	99.7	2141	12	AAQ22215	Type 1 TNF receptor
22	479.8	99.3	2170	14	AAQ50870	p55 Tumour necrosi
23	478.4	99.0	509	13	AAQ24441	Encodes truncated
24	475	98.3	1117	18	AAQ19321	cDNA for TNF(2019
25	424.4	87.9	1049	19	AAQ19321	cDNA for TNF(2019
26	424.4	87.9	1202	18	AAQ19321	cDNA for TNF(2019
27	415	85.9	1574	21	AAQ50196	Male fusion plasmid
28	403	79.3	504	13	AAQ24445	Encodes truncated
29	357.2	74.0	474	13	AAQ24445	Encodes truncated
30	312.2	64.5	339	19	AAQ19803	Truncated TNFR, S
31	308	63.8	333	19	AAQ19805	Truncated TNFR, S
32	294.2	62.0	332	19	AAQ19807	Truncated TNFR, S
33	299.2	61.9	5870	21	AAQ15944	Nucleotide sequenc
34	297.4	61.6	2173	11	AAQ06284	Rat Tumour Necrosi
35	294.6	61.0	315	19	AAQ19806	Truncated TNFR, S
36	273.8	56.7	294	19	AAQ19808	Truncated TNFR, S
37	264.6	54.8	295	19	AAQ19807	Truncated TNFR, S
38	258	53.4	1497	21	AAQ250194	Male fusion plasmid
39	257.8	53.4	477	13	AAQ24444	Encodes truncated
40	250.8	51.9	1464	21	AAQ50195	Male fusion plasmid
41	221.8	45.7	362	13	AAQ24443	Encodes truncated
42	152.8	31.6	1358	21	AAQ95103	Partial human TNFR
43	132.4	27.4	1027	12	AAQ10878	Partial sequence o
44	132.4	27.4	1027	22	AAQ93643	Gene for TNF-R
45	58	12.0	2254	21	AAQ95104	Partial human TNFR

ALIGNMENTS

RESULT	1
AAQ1548	
10	AAQ1548 standard: cDNA: 483 bp.
XX	AAQ1548:
XX	28-SEP-1998 (first entry)
XX	Human soluble tumour necrosis factor receptor type I
XX	Human, tumour necrosis factor, TNF-R receptor type I
XX	Human, tumour necrosis factor, TNF-R binding protein
XX	Gene for TNF-R type I
XX	Human sapiens.
XX	US
XX	Key
XX	CDS
XX	Location/Qualifiers
XX	1..483
XX	/std-a
XX	/product: "human soluble TNF receptor type I"
XX	WO9824463-A2.
XX	11-JUN-1998.
XX	08-DEC-1997: 97W-9522733.
XX	99-JUN-1997: 97W-9522733.
XX	96-DEC-1996: 96US-0032587.
XX	23-JAN-1997: 96US-0036355.
XX	07-FEB-1997: 96US-0039315.
XX	(AMCIP) AMCHN TNF.

PA (AMGE-) AMGEN INC.
 XX Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
 PI Vanderslice RW, Vannice J, Kohno T;
 XX WPI: 2001-006443/01.
 DR P-PSDB; AAB37676.
 XX Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
 PT non-native cysteine residue cross-linked with polyethylene glycol,
 FT useful for treating inflammatory and degenerative diseases mediated by
 TNF -
 XX Example 6; Fig 20; 82pp; English.
 XX The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
 CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
 CC novel TNF inhibitors of the present invention are useful as therapeutic
 CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
 CC for treating inflammatory and degenerative diseases mediated by TNF. The
 CC present sequence is the coding sequence for the 30 kDa TNF inhibitor
 CC The 30 kDa TNF inhibitor can inhibit TNF alpha.
 XX Sequence 483 BP; 130 A; 124 C; 123 G; 106 T; 0 other;

Query Match 100.0%; Score 483; DB 22; Length 483;
 Best Local Similarity 100.0%; Pred. No. 3.4e-141;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 gatagtgtgtgtcccaaggaaataatataccacctcaaaataattcgtgtgac 60
 DB 1 gatagtgtgtgtcccaaggaaataatataccacctcaaaataattcgtgtgac 60
 QY 61 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 120
 DB 61 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 120
 QY 121 taccaggaatgtgaagagagagagagagagagagagagagagagagagagag 180
 DB 121 taccaggaatgtgaagagagagagagagagagagagagagagagagagagag 180
 QY 181 agctgtcccaaatgccgaagaaatgggttcaggtgagagatctcttgcacatgac 240
 DB 181 agctgtcccaaatgccgaagaaatgggttcaggtgagagatctcttgcacatgac 240
 QY 241 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 300
 DB 241 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 300
 QY 301 taccaggaatgtgaagagagagagagagagagagagagagagagagagagag 360
 DB 301 taccaggaatgtgaagagagagagagagagagagagagagagagagagagag 360
 QY 361 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 420
 DB 361 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 420
 QY 421 taccaggaatgtgaagagagagagagagagagagagagagagagagagagag 480
 DB 421 taccaggaatgtgaagagagagagagagagagagagagagagagagagagag 480
 QY 481 aat 483
 DB 481 aat 483

RESULT 5
 AAT94022
 ID AAT94022 standard; cDNA; 1301 BP.
 XX
 AC AAT94022;
 XX

DT 19-MAR-1998 (first entry)
 XX
 DE CDNA for TBE(20-190)/hCG-beta fusion protein.
 XX
 KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
 KW beta subunit; hCG-beta; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 279..1289
 FT /*tag= a
 XX
 XX W09730161-A1.
 XX
 XX 21-AUG-1997.
 XX
 XX 20-FEB-1997; 97WO-US02315.
 XX
 XX 20 FEB 1996; 96US-0011936.
 XX
 XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 XX
 XX Campbell RK, Chappel SC, Jameson BA.
 XX
 XX WPI: 1997-425036/39.
 DR P-PSDB; AAB33360.
 XX
 XX Hybrid dimeric protein comprising two co-expressed units - each
 PT based on receptor or ligand and a subunit of a heterodimeric
 PT hormone, especially FSH, for inducing follicular maturation
 XX
 XX Example; Pages 39-40, 60pp, English.
 XX
 XX A novel fusion protein comprises a dimer forming co-expressed amino
 CC acid sequences, each consisting of a homodimeric or heterodimeric
 CC receptor chain of ligand, with ligand receptor binding activity,
 CC bound directly or via a peptide linker to a subunit of a
 CC heterodimeric protein hormone capable of forming a heterodimer with
 CC the hormone's other subunits. The fusion protein, e.g. the
 CC thrombopoietin (TPO)/human chorionic gonadotrophin beta subunit
 CC (hCG-beta) fusion protein encoded by the present sequence,
 CC significantly increases the biological activity of the hormone
 CC component, reducing the requirement for hormone itself and the
 CC number of injections needed.
 XX
 XX Sequence 1301 BP, 259 A, 413 C, 451 G, 268 T; 0 other;

Query Match 100.0%; Score 483; DB 18; Length 1301;
 Best Local Similarity 100.0%; Pred. No. 5.4e-141;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 gatagtgtgtgtcccaaggaaataatataccacctcaaaataattcgtgtgac 60
 DB 345 gatagtgtgtgtcccaaggaaataatataccacctcaaaataattcgtgtgac 404
 QY 61 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 120
 DB 405 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 464
 QY 121 taccaggaatgtgaagagagagagagagagagagagagagagagagagagag 180
 DB 465 taccaggaatgtgaagagagagagagagagagagagagagagagagagagag 524
 QY 181 agctgtcccaaatgccgaagaaatgggttcaggtgagagatctcttgcacatgac 240
 DB 525 agctgtcccaaatgccgaagaaatgggttcaggtgagagatctcttgcacatgac 584
 QY 241 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 300
 DB 585 aatgccacaaaggaaacctacttctgataataaactgacggccggagagataaac 644

KW autoimmune disease; rheumatoid arthritis

OS Homo sapiens

XX Key: Location/Qualifiers

FT CDS 156..1517

FT /product= human TNF-alpha

FT /tag= a

FT /tag= b

FT /note= #3

FT /tag= c

FT /tag= d

FT /tag= e

FT /tag= f

FT /tag= g

FT /tag= h

FT /tag= i

FT /tag= j

FT /tag= k

FT /tag= l

FT /tag= m

FT /tag= n

FT /tag= o

FT /tag= p

FT /tag= q

FT /tag= r

FT /tag= s

FT /tag= t

FT /tag= u

FT /tag= v

FT /tag= w

FT /tag= x

FT /tag= y

FT /tag= z

FT /tag= AA

FT /tag= AB

FT /tag= AC

FT /tag= AD

FT /tag= AE

FT /tag= AF

FT /tag= AG

FT /tag= AH

FT /tag= AI

XX Query Match 100.0%; Score 483; DB 13; Length 2062;

XX Best Local Similarity 100.0%; Pred. No. 6.5e-141;

XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 qatagtagtgcctcccaagaaataatatacccccctcaaaataattccatttgcgtgacc 60

XX 275 qataatgtagtgcctcccaagaaataatatacccccctcaaaataattccatttgcgtgacc 334

XX 61 agtggcccaagaaataatatacccccctcaaaataattccatttgcgtgacc 120

XX 156..1517

XX /product= human TNF-alpha

XX /tag= a

XX /tag= b

XX /note= #3

XX /tag= c

XX /tag= d

XX /tag= e

XX /tag= f

XX /tag= g

XX /tag= h

XX /tag= i

XX /tag= j

XX /tag= k

XX /tag= l

XX /tag= m

XX /tag= n

XX /tag= o

XX /tag= p

XX /tag= q

XX /tag= r

XX /tag= s

XX /tag= t

XX /tag= u

XX /tag= v

XX /tag= w

XX /tag= x

XX /tag= y

XX /tag= z

XX /tag= AA

XX /tag= AB

XX /tag= AC

XX /tag= AD

XX /tag= AE

XX /tag= AF

RESULT 12

AAQ10883

ID: AAQ10883 standard; cDNA; 2088 bp.

XX AC AAQ10883;

XX 13-MAY-1991 (first entry)

XX 30kd TNF inhibitor precursor gene in lambda-qt10-7ctn1bp.

XX Tumour necrosis factor; inhibitor; ss.

XX Homo sapiens.

XX Key: Location/Qualifiers

XX CDS 171..1536

XX /tag= a

XX AU058976-A.

XX 24-JAN-1991.

XX 16-JUL-1990; 90AQ-0059976.

XX 07-FEB-1990; 90BS-0474661.

XX 18-JUL-1989; 89BS-0381080.

XX 11-DEC-1989; 89BS-0450329.

XX (SYNPE-) SYNPROGEN INC.

XX WPI; 1991-073847/11.

XX P-PSDB; AAR10986.

XX Tumour necrosis factor inhibitor - for suppression of TNF alpha

XX and -beta, useful as therapeutic agent.

XX Disclosure; Fig 21; 142bp; English.

XX The sequence encodes the entire 30 kD TNF inhibitor. The clone from

XX which the sequence was obtained, was isolated from a cDNA library

XX prep. from RMA form 5917 cells treated with IFN-gamma. The whole

XX gene can be inserted into expression vectors for prep. of TNF

cc necrosis factor (TNF). The products of the invention have
cc anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
cc to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
cc glomerulonephritis, cerebral malaria, immune responses and inflammation),
cc (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
cc diagnostic determination of TNF in body fluids. Antibodies raised against
cc (I) are used for affinity purification of (I). This sequence encodes
cc a tumour necrosis factor binding protein described in the method of
cc the invention.
xx
SQ Sequence 2111; HF, 445 A, 629 C, 587 G, 450 T, 0 other;

Query Match 100.0%; Score 483; DB 20; Length 2111;
Best local Similarity 100.0%; Pred. No. 6,60-141;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 qataatqatqatcccaagaaataatataaccaccccaaaaataatcgaatttgcgtacc 60
Db 307 qataatqatqatcccaagaaataatataaccaccccaaaaataatcgaatttgcgtacc 366
QY 61 aagtaaccacaaagaaactacttgtaaatgaatctcagggccggaggaagatacggac 120
Db 367 aagtgccacaaagaaactacttgtaaatgaatctcagggccggaggaagatacggac 426
QY 121 tcaaggaatqataagagcggctccttcacgcgttcagaataaccacccctcagacacggctc 180
Db 427 tgcaggagtgtagagcggctccttcacgcgttcagaataaccacccctcagacacggctc 486
QY 181 agctgctcccaatgcccaaaagaaatagatcagatggaacatctctttacacaaatgac 240
Db 487 agctgctcccaatgcccaaaagaaatagatcagatggaacatctctttacacaaatgac 546
QY 241 cggacacccgtgtggtgcaggaagaaacagtaaccgcaattattggagtgaaacacctt 300
Db 547 cggacacccgtgtggtgcaggaagaaacagtaaccgcaattattggagtgaaacacctt 606
QY 301 ttcaatgcttcaatcagaacctctaccccaatgggaacccgtgacacctctcctggccaggag 360
Db 607 ttcaatgcttcaatcagaacctctaccccaatgggaacccgtgacacctctcctggccaggag 666
QY 361 aaacaaacacccgtgtgacctgacctgacctgtttcttctaaagaaacaaacagatgatac 420
Db 667 aaacaaacacccgtgtgacctgacctgacctgtttcttctaaagaaacaaacagatgatac 726
QY 421 tctgtatgaactatataagaaagccctggagtgacagaaattgtgacctacccagattgag 480
Db 727 tctgtatgaactatataagaaagccctggagtgacagaaattgtgacctacccagattgag 786
QY 481 aat 483
Db 787 aat 784

Search completed: April 24, 2002, 9:28:29
Job time: 3407 sec